

SEQUENCE LISTING

<110> Seeley, Todd W.

<120> h1BUB3 GENE INVOLVED IN HUMAN CANCERS

<130> PP-01406.004/200130.438D1

<140> US

<141> 2002-02-27

<160> PP

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapien

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 42121: PRT
 42131: Homo sapien

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0011: 3441

0012: DNA

0013: Homo sapien

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0210: 4

0211: 1035

0212: PRT

0213: Homo sapien

0430: 4

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c214> 11 c215> 26 c216> DNA c217> Artificial Sequence	
c218> c219> PCR primer	
c401> 11 aaccttag tgcctggaga cggct	26
c210> 11 c211> 2- c212> DNA c213> Artificial Sequence	
c214> c215> PCR primer	
c402> 11 agabgtttc caaacaagca gggttatg	23
c210> 13 c211> 3- c212> DNA c213> Artificial Sequence	
c214> c215> PCR primer	
c403> 13 tgaatgat aat aaaacaattc gtactcccca	30
c210> 14 c211> 22 c212> DNA c213> Artificial Sequence	
c214> c215> PCR primer	
c404> 14 gactcaaaca atttgcctt ctggtatca	29

<210> 15
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Sense PCR primer

<400> 15
 tttctccag atgaccgggtt ctaacga 27

<100> 16
 <110> 10
 <120> DNA
 <130> Homo sapien

<400> 16
 ttaattccac 10

<100> 17
 <110> 10
 <120> DNA
 <130> Homo sapien

<400> 17
 ttttaagt tca 10

<210> 18
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> PCR primer

<400> 18
 tttttggagg tccacctaat catcctgtga aagtgggt 38

<100> 19
 <110> 30
 <120> DNA
 <130> Artificial Sequence

<220>
 <221> PCR primer

<400> 19
 actaagggaac agaaggggaa atacgtcaga ctact 35

<100> 20
 <210> 31
 <212> DNA
 <213> Artificial Sequence

<220>

<223> PCR primer

<210> 13

tttgggtaaa caaaattgga gggcaagtga c

31

<210> 21

<211> 32

<212> DNA

<213> Artificial Sequence

<214>

<215> PCR primer

<210> 21

tttttcaaaa gaaacaaatg gctcagcagc ct

32

<210> 33

<211> 34

<212> DNA

<213> Artificial Sequence

<214>

<215> PCR primer

<210> 34

tctcagtgca cctaatacatc ctgtgaaagt gggt

34

<210> 35

<211> 35

<212> DNA

<213> Artificial Sequence

<214>

<215> PCR primer

<210> 37

attttttggg aaatacgtca gactactgta caggg

35

<210> 34

<211> 37

<212> PET

<213> Homo sapien

<1000> 24

Asp Tyr Lys Asp Asp Asp Lys

1

5

<210> 38

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 25

atcaagaggagg tcattgccct tgtagctctg catgt

35

<210> 26

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 26

ttatccagag ttctctggga gctctgtggc tgatt

35

<210> 27

<211> 230

<212> PRT

<213> Homo sapien

<400> 27

Met	Thr	Gly	Ser	Asn	Glu	Phe	Lys	Leu	Asn	Gln	Pro	Pro	Glu	Asp	Gly
1				5					10				15		
Ile	Ser	Ser	Val	Lys	Phe	Ser	Pro	Asn	Thr	Ser	Gln	Phe	Leu	Leu	Val
			20					25				30			
Ser	Ser	Trp	Asp	Thr	Ser	Val	Arg	Leu	Tyr	Asp	Val	Pro	Ala	Asn	Ser
		35					40				45				
Met	Arg	Leu	Lys	Tyr	Gln	His	Thr	Gly	Ala	Val	Leu	Asp	Cys	Ala	Phe
	50					55				60					
Tyr	Asp	Pro	Thr	His	Ala	Trp	Ser	Gly	Gly	Leu	Asp	His	Gln	Leu	Lys
	65				70				75					80	
Met	His	Asp	Leu	Asn	Thr	Asp	Gln	Glu	Asn	Leu	Val	Gly	Thr	His	Asp
			85					90					95		
Ala	Pro	Ile	Arg	Cys	Val	Glu	Iyr	Cys	Pro	Glu	Val	Asn	Val	Met	Val
		100					105					110			
Thr	Gly	Ser	Trp	Asp	Gln	Thr	Val	Lys	Leu	Trp	Asp	Pro	Arg	Thr	Pro
	115						120					125			
Cys	Asn	Ala	Gly	Thr	Phe	Ser	Gln	Pro	Glu	Lys	Val	Tyr	Thr	Leu	Ser
	130					135					140				
Val	Ser	Gly	Asp	Arg	Leu	Ile	Val	Gly	Thr	Ala	Gly	Arg	Arg	Val	Leu
	145				150				155					160	
Val	Trp	Asp	Leu	Arg	Asn	Met	Gly	Tyr	Val	Gln	Gln	Arg	Arg	Glu	Ser
			165				170					175			
Ser	Leu	Lys	Tyr	Gln	Thr	Arg	Cys	Ile	Arg	Ala	Phe	Pro	Asn	Lys	Gln
		180				185					190				
Gly	Tyr	Val	Leu	Ser	Ser	Ile	Glu	Gly	Arg	Val	Ala	Val	Glu	Tyr	Leu
	195					200					205				
Asp	Pro	Ser	Pro	Glu	Val	Gln	Lys	Lys	Lys	Tyr	Ala	Phe	Lys	Cys	His
	210					215					220				
Arg	Leu	Lys	Glu	Asn	Asn	Ile	Glu	Gln	Ile	Tyr	Pro	Val	Asn	Ala	Ile
	225			230					235					240	
Ser	Phe	His	Asn	Ile	His	Asn	Thr	Phe	Ala	Thr	Gly	Gly	Ser	Asp	Gly

				245					250					255			
Phe	Val	Asn	Ile	Trp	Asp	Pro	Phe	Asn	Lys	Lys	Arg	Leu	Cys	Gln	Phe		
			260					265					270				
His	Arg	Tyr	Pro	Thr	Ser	Ile	Ala	Ser	Leu	Ala	Phe	Ser	Asn	Asp	Gly		
		275					280				285						
Thr	Thr	Leu	Ala	Ile	Ala	Ser	Ser	Tyr	Met	Tyr	Glu	Met	Asp	Asp	Thr		
	290					295				300							
Val	His	Pro	Glu	Asp	Gly	Ile	Phe	Ile	Arg	Gln	Val	Thr	Asp	Ala	Glu		
305				310					315						320		
Thr	Lys	Pro	Lys	Val	His	Leu	Ile	Ile	Leu								
			325					330									

0110> 28

0111> 341

0112> PRT

0113> Saccharomyces cerevisiae

0100> 28

Met	Gln	Ile	Val	Gln	Ile	Glu	Gln	Ala	Pro	Lys	Asp	Tyr	Ile	Ser	Asp		
			5					10						15			
Ile	Lys	Ile	Ile	Pro	Ser	Lys	Ser	Leu	Leu	Leu	Ile	Thr	Ser	Trp	Asp		
		20					25					30					
Gly	Ser	Leu	Thr	Val	Tyr	Lys	Phe	Asp	Ile	Gln	Ala	Lys	Asn	Val	Asp		
	35					40				45							
Leu	Leu	Gln	Ser	Leu	Arg	Tyr	Lys	His	Pro	Leu	Leu	Cys	Cys	Asn	Phe		
	50				55				60								
Ile	Asp	Asn	Thr	Asp	Leu	Gln	Ile	Tyr	Val	Gly	Thr	Val	Gln	Gly	Glu		
65			70				75							80			
Ile	Leu	Lys	Val	Asp	Leu	Ile	Gly	Ser	Pro	Ser	Phe	Gln	Ala	Leu	Thr		
		85					90							95			
Asn	Asn	Glu	Ala	Asn	Leu	Gly	Ile	Cys	Arg	Ile	Cys	Lys	Tyr	Gly	Asp		
	100					105							110				
Asp	Lys	Leu	Ile	Ala	Ala	Ser	Trp	Asp	Gly	Leu	Ile	Glu	Val	Ile	Asp		
	115					120						125					
Pro	Arg	Asn	Tyr	Gly	Asp	Gly	Val	Ile	Ala	Val	Lys	Asn	Leu	Asn	Ser		
	130				135						140						
Asn	Asn	Thr	Lys	Val	Lys	Asn	Lys	Ile	Phe	Thr	Met	Asp	Thr	Asn	Ser		
	145			150					155					160			
Ser	Arg	Leu	Ile	Val	Gly	Met	Asn	Asn	Ser	Gln	Val	Gln	Trp	Phe	Arg		
		165					170						175				
Leu	Pro	Leu	Cys	Glu	Asp	Asp	Asn	Gly	Thr	Ile	Glu	Glu	Ser	Gly	Leu		
	180						185						190				
Lys	Tyr	Gln	Ile	Arg	Asp	Val	Ala	Leu	Leu	Pro	Lys	Glu	Gln	Glu	Gly		
	195					200						205					
Tyr	Ala	Cys	Ser	Ser	Ile	Asp	Gly	Arg	Val	Ala	Val	Glu	Phe	Phe	Asp		
	210					215					220						
Asp	Gln	Gly	Asp	Asp	Tyr	Asn	Ser	Ser	Lys	Arg	Phe	Ala	Phe	Arg	Cys		
225				230						235					240		
His	Arg	Leu	Asn	Leu	Lys	Asp	Thr	Asn	Leu	Ala	Tyr	Pro	Val	Asn	Ser		
		245						250					255				
Ile	Glu	Phe	Ser	Pro	Arg	His	Lys	Phe	Leu	Tyr	Thr	Ala	Gly	Ser	Asp		
	260						265						270				
Gly	Ile	Ile	Ser	Cys	Trp	Asn	Leu	Gln	Thr	Arg	Lys	Lys	Ile	Lys	Asn		
	275					280						285					

Phe Ala Lys Phe Asn Glu Asp Ser Val Val Lys Ile Ala Cys Ser Asp
 290 295 300
 Asn Ile Leu Cys Leu Ala Thr Ser Asp Asp Thr Phe Lys Thr Asn Ala
 305 310 315 320
 Ala Ile Asp Gln Thr Ile Glu Leu Asn Ala Ser Ser Ile Tyr Ile Ile
 325 330 335
 Phe Asp Tyr Glu Asn
 340

0210 - .9
 0211 - 026
 0212 - PRT
 0213 - Mus musculus

0400 - .9
 Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly
 1 5 10 15
 Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val
 20 25 30
 Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
 35 40 45
 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 50 55 60
 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
 65 70 75 80
 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
 85 90 95
 Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Glu Val Asn Val Met Val
 100 105 110
 Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp Pro Arg Thr Pro
 115 120 125
 Lys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val Tyr Thr Leu Ser
 130 135 140
 Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly Arg Arg Val Leu
 145 150 155 160
 Val Trp Asp Leu Trp Asn Met Gly Tyr Val Gln Gln Arg Arg Glu Ser
 165 170 175
 Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe Pro Asn Lys Gln
 180 185 190
 Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala Val Glu Tyr Leu
 195 200 205
 Asp Pro Ser Pro Glu Val Gln Lys Lys Lys Tyr Ala Phe Lys Cys His
 210 215 220
 Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro Val Asn Ala Ile
 225 230 235 240
 Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly Gly Ser Asp Gly
 245 250 255
 Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg Leu Cys Gln Phe
 260 265 270
 His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe Ser Asn Asp Gly
 275 280 285
 Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu Met Asp Asp Thr
 290 295 300
 Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val Thr Asp Ala Gln

305 310
 Thr Lys Pro Lys Ser Thr
 325

315

320

0110: 30
 0111: 368
 0112: PRT
 0113: Homo sapien

0400: 30

Met	Ser	Leu	Phe	Gly	Thr	Thr	Ser	Gly	Phe	Gly	Thr	Ser	Gly	Thr	Ser
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Met	Phe	Gly	Ser	Ala	Thr	Thr	Asp	Asn	His	Asn	Pro	Met	Lys	Asp	Ile
		20					25						30		
Ala	Val	Thr	Ser	Ser	Pro	Asp	Asp	Ser	Ile	Gly	Cys	Leu	Ser	Phe	Ser
	35					40						45			
Pro	Pro	Thr	Leu	Pro	Gly	Asn	Phe	Leu	Ile	Ala	Gly	Ser	Trp	Ala	Asn
	50					55					60				
Asp	Val	Arg	Cys	Trp	Gln	Val	Gln	Asp	Ser	Gly	Gln	Thr	Ile	Pro	Lys
		70						75						80	
Ala	Gln	Gln	Met	His	Thr	Gly	Pro	Val	Leu	Asp	Val	Cys	Trp	Ser	Asp
			85					90						95	
Asp	Gly	Ser	Lys	Val	Phe	Thr	Ala	Ser	Cys	Asp	Lys	Thr	Ala	Lys	Met
		100						105					110		
Trp	Asp	Leu	Ser	Ser	Asn	Gln	Ala	Ile	Gln	Ile	Ala	Gln	His	Asp	Ala
		115					120						125		
Pro	Val	Lys	Thr	Ile	His	Trp	Ile	Lys	Ala	Pro	Asn	Tyr	Ser	Cys	Val
	130					135						140			
Met	Thr	Gly	Ser	Trp	Asp	Lys	Thr	Leu	Lys	Phe	Trp	Asp	Thr	Arg	Ser
	145				150					155					160
Ser	Asn	Pro	Met	Met	Val	Leu	Gln	Leu	Pro	Glu	Arg	Cys	Tyr	Cys	Ala
			165					170						175	
Asp	Val	Ile	Tyr	Pro	Met	Ala	Val	Val	Ala	Thr	Ala	Glu	Arg	Gly	Leu
		180						185					190		
Ile	Val	Tyr	Gln	Leu	Glu	Asn	Gln	Pro	Ser	Glu	Phe	Arg	Arg	Ile	Glu
	195						200					205			
Ser	Pro	Leu	Lys	His	Gln	His	Arg	Cys	Val	Ala	Ile	Phe	Lys	Asp	Lys
	210					215						220			
Gln	Asn	Lys	Pro	Thr	Gly	Phe	Ala	Leu	Gly	Ser	Ile	Glu	Gly	Arg	Val
	225				230					235					240
Ala	Ile	His	Tyr	Ile	Asn	Pro	Pro	Asn	Pro	Ala	Lys	Asp	Asn	Phe	Thr
		245						250						255	
Phe	Lys	Cys	His	Arg	Ser	Asn	Gly	Thr	Asn	Thr	Ser	Ala	Pro	Gln	Asp
		260					265						270		
Ile	Tyr	Ala	Val	Asn	Gly	Ile	Ala	Phe	His	Pro	Val	His	Gly	Thr	Leu
	275					280						285			
Ala	Thr	Val	Gly	Ser	Asp	Gly	Arg	Phe	Ser	Phe	Trp	Asp	Lys	Asp	Ala
	290					295					300				
Arg	Thr	Lys	Leu	Lys	Thr	Ser	Glu	Gln	Leu	Asp	Gln	Pro	Ile	Ser	Ala
	305					310				315					320
Cys	Cys	Phe	Asn	His	Asn	Gly	Asn	Ile	Phe	Ala	Tyr	Ala	Ser	Ser	Tyr
			325						330					335	
Asp	Trp	Ser	Lys	Gly	His	Glu	Phe	Tyr	Asn	Pro	Gln	Lys	Lys	Asn	Tyr
		340						345						350	

Ile Phe Leu Arg Asn Ala Ala Glu Glu Leu Lys Pro Arg Asn Lys Lys
 355 360 365

4210> 31

4211> 352

4212> PRT

4213> Schizosaccharomyces pombe

4400> 31

Met Ser Leu Phe Gly Gln Ala Thr Thr Ser Thr Val Ser Asn Ala Thr
 1 5 10 15
 Gly Asp Leu Lys Lys Asp Val Glu Val Ala Gln Pro Pro Glu Asp Ser
 20 25 30
 Ile Ser Asp Leu Ala Phe Ser Pro Gln Ala Glu Tyr Leu Ala Ala Ser
 35 40 45
 Ser Trp Asp Ser Lys Val Arg Ile Tyr Glu Val Gln Ala Thr Gly Gln
 50 55 60
 Ser Ile Gly Lys Ala Leu Tyr Glu His Gln Gly Pro Val Leu Ser Val
 65 70 75 80
 Asn Trp Ser Arg Asp Gly Thr Lys Val Ala Ser Gly Ser Val Asp Lys
 85 90 95
 Ser Ala Lys Val Phe Asp Ile Gln Thr Gly Gln Asn Gln Gln Val Ala
 100 105 110
 Ala His Asp Asp Ala Val Arg Cys Val Arg Phe Val Glu Ala Met Gly
 115 120 125
 Thr Ser Pro Ile Leu Ala Thr Gly Ser Trp Asp Lys Thr Leu Lys Tyr
 130 135 140
 Trp Asp Leu Arg Gln Ser Thr Pro Ile Ala Thr Val Ser Leu Pro Glu
 145 150 155 160
 Arg Val Tyr Ala Met Asp Cys Val His Pro Leu Leu Thr Val Ala Thr
 165 170 175
 Ala Glu Arg Asn Ile Cys Val Ile Asn Leu Ser Glu Pro Thr Lys Ile
 180 185 190
 Phe Lys Leu Ala Met Ser Pro Leu Lys Phe Gln Thr Arg Ser Leu Ala
 195 200 205
 Cys Phe Ile Lys Gly Asp Gly Tyr Ala Ile Gly Ser Val Glu Gly Arg
 210 215 220
 Cys Ala Ile Gln Asn Ile Asp Glu Lys Asn Ala Ser Gln Asn Phe Ser
 225 230 235 240
 Phe Arg Cys His Arg Asn Gln Ala Gly Asn Ser Ala Asp Val Tyr Ser
 245 250 255
 Val Asn Ser Ile Ala Phe His Pro Gln Tyr Gly Thr Phe Ser Thr Ala
 260 265 270
 Gly Ser Asp Gly Thr Phe Ser Phe Trp Asp Lys Asp Ser His Gln Arg
 275 280 285
 Leu Lys Ser Tyr Pro Asn Val Gly Gly Thr Ile Ser Cys Ser Thr Phe
 290 295 300
 Asn Arg Thr Gly Asp Ile Phe Ala Tyr Ala Ile Ser Tyr Asp Trp Ser
 305 310 315 320
 Lys Gly Tyr Thr Phe Asn Asn Ala Gln Leu Pro Asn Lys Ile Met Leu
 325 330 335
 His Pro Val Pro Gln Asp Glu Ile Lys Pro Arg Pro Lys Lys Gly Arg
 340 345 350

<210> 32
 <211> 365
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 32

Met	Ser	Phe	Phe	Asn	Arg	Ser	Asn	Thr	Thr	Ser	Ala	Leu	Gly	Thr	Ser	1	5	10	15
Thr	Ala	Met	Ala	Asn	Glu	Lys	Asp	Leu	Ala	Asn	Asp	Ile	Val	Ile	Asn	20	25	30	35
Ser	Pro	Ala	Glu	Asp	Ser	Ile	Ser	Asp	Ile	Ala	Phe	Ser	Pro	Gln	Gln	40	45	50	55
Asp	Phe	Met	Phe	Ser	Ala	Ser	Ser	Trp	Asp	Gly	Lys	Val	Arg	Ile	Trp	60	65	70	75
Asp	Val	Gln	Asn	Gly	Val	Pro	Gln	Gly	Arg	Ala	Gln	His	Glu	Ser	Ser	80	85	90	95
Ser	Pro	Val	Leu	Cys	Thr	Arg	Trp	Ser	Asn	Asp	Gly	Thr	Lys	Val	Ala	100	105	110	115
Ser	Gly	Gly	Cys	Asp	Asn	Ala	Leu	Lys	Leu	Tyr	Asp	Ile	Ala	Ser	Gly	120	125	130	135
Gln	Thr	Gln	Gln	Ile	Gly	Met	His	Ser	Ala	Pro	Ile	Lys	Val	Leu	Arg	140	145	150	155
Phe	Val	Gln	Cys	Gly	Pro	Ser	Asn	Thr	Gln	Cys	Ile	Val	Thr	Gly	Ser	160	165	170	175
Trp	Asp	Lys	Thr	Ile	Lys	Tyr	Trp	Asp	Met	Arg	Gln	Pro	Gln	Pro	Val	180	185	190	195
Ser	Thr	Val	Met	Met	Pro	Glu	Arg	Val	Tyr	Ser	Met	Asp	Asn	Lys	Gln	200	205	210	215
Ser	Leu	Leu	Val	Val	Ala	Thr	Ala	Glu	Arg	His	Ile	Ala	Ile	Ile	Asn	220	225	230	235
Leu	Ala	Asn	Pro	Thr	Thr	Ile	Phe	Lys	Ala	Thr	Thr	Ser	Pro	Leu	Lys	240	245	250	255
Trp	Gln	Thr	Asp	Cys	Val	Ala	Cys	Tyr	Asn	Glu	Ala	Asp	Gly	Tyr	Ala	260	265	270	275
Ile	Gly	Ser	Val	Glu	Gly	Arg	Cys	Ser	Ile	Arg	Tyr	Ile	Asp	Asp	Gly	280	285	290	295
Met	Gln	Lys	Lys	Ser	Gly	Phe	Ser	Phe	Lys	Cys	His	Arg	Gln	Thr	Asn	300	305	310	315
Pro	Asn	Arg	Ala	Pro	Gly	Ser	Asn	Gly	Gln	Ser	Leu	Val	Tyr	Pro	Val	320	325	330	335
Asn	Ser	Ile	Ala	Phe	His	Pro	Leu	Tyr	Gly	Thr	Phe	Val	Thr	Ala	Gly	340	345	350	355
Gly	Asp	Gly	Thr	Phe	Asn	Phe	Trp	Asp	Lys	Asn	Gln	Arg	His	Arg	Leu	360	365	370	375
Lys	Gly	Tyr	Pro	Thr	Leu	Gln	Ala	Ser	Ile	Pro	Val	Cys	Ser	Phe	Asn	380	385	390	395
Arg	Asn	Gly	Ser	Val	Phe	Ala	Tyr	Ala	Leu	Ser	Tyr	Asp	Trp	His	Gln	400	405	410	415
Gly	His	Met	Gly	Asn	Arg	Pro	Asp	Tyr	Pro	Asn	Val	Ile	Arg	Leu	His	420	425	430	435
Ala	Thr	Thr	Asp	Glu	Glu	Val	Lys	Glu	Lys	Lys	Lys	Arg				440	445	450	455